

### **Abstract of the Disclosure**

The invention relates to a compound that competitively inhibits binding of CSP to *S. mutans* histidine kinase. The compound is preferably a peptide or an antibody. The compound is preferably a derivative of [SEQ ID NO:2], a fragment of [SEQ ID NO:2] or a derivative of a fragment of [SEQ ID NO:2].

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43153.01 1889-00401

SEQUENCE LISTING

<110> CVITKOVITCH, Dennis

<120> SIGNAL PEPTIDES NUCLEIC ACID MOLECULES AND METHODS FOR TREATMENT OF CAVITIES

<130> 311/0003

<140> 2 302 861

<141> 2000-04-10

<160> 28

<170> PatentIn version 3.0

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<211> 141

<212> DNA

<213> Streptococcus mutans

<220>

<221> CDS

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gat gaa tta gag att atc att ggc gga agc gga agc cta tca aca ttt 96  
Asp Glu Leu Glu Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe  
20 25 30

ttc cgg ctg ttt aac aga agt ttt aca caa gct ttg gga aaa taa 141  
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Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys  
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1 5 10 15

acc gtt cta ttt ctc ttg ttt cta ttt tct aag gta agt aat gtc act 96  
Thr Val Leu Phe Leu Leu Phe Leu Phe Ser Lys Val Ser Asn Val Thr  
20 25 30

tta tcg aaa aag gaa tta act ctt ttt tcg ata agc aat ttt ctg ata 144  
Leu Ser Lys Lys Glu Leu Thr Leu Phe Ser Ile Ser Asn Phe Leu Ile  
35 40 45

atg att gct gtt acg atg gtg aac gta aac ctg ttt tat cct gca gag 192  
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50 55 60

cct ctt tat ttt ata gct tta tca att tat ctt aat aga cag aat agt 240  
Pro Leu Tyr Phe Ile Ala Leu Ser Ile Tyr Leu Asn Arg Gln Asn Ser  
65 70 75 80

ctt tct cta aat ata ttt tat ggt ctg ctg cct gtt gcc agt tct gac 288  
Leu Ser Leu Asn Ile Phe Tyr Gly Leu Leu Pro Val Ala Ser Ser Asp  
85 90 95

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Ile Val Met Gly Ser Ser Ile Ile Thr Thr Tyr Met Ile Glu Phe Ala			
115	120	125	
gga ata gcg cta agt tac ctc ttt ctc agt gtg ttc aat gtt gat att		432	
Gly Ile Ala Leu Ser Tyr Leu Phe Leu Ser Val Phe Asn Val Asp Ile			
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ttg tat gtt ata gag agt tat aat gtg ata ccg act tta aaa ttt cgt		576	
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Gln Lys Glu Ala Gln Ile Arg Asn Ile Thr Gln Tyr Ser Gln Gln Ile			
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Glu Ser Leu Tyr Lys Asp Ile Arg Ser Phe Arg His Asp Tyr Leu Asn			
245	250	255	
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260	265	270	
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Gln Asp Thr Arg Tyr Asn Ile Gly His Leu Ala Asn Ile Gln Asn Asp			
290	295	300	
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Lys Ile Ala Val Asn Val Glu Val Ser Ser Lys Ile Gln Leu Pro Glu			

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aaa gaa aaa caa ata gat gtg agt aaa att ttt aaa gaa aac tat tcc Lys Glu Lys Gln Ile Asp Val Ser Lys Ile Phe Lys Glu Asn Tyr Ser 385	390	395	1200
act aaa ggc tcc aat cgc ggt att ggt tta gca aag gtg aat cat att Thr Lys Gly Ser Asn Arg Gly Ile Gly Leu Ala Lys Val Asn His Ile 405	410	415	1248
ctt gaa cat tat ccc aaa acc agt tta caa aca agc aat cat cat cat Leu Glu His Tyr Pro Lys Thr Ser Leu Gln Thr Ser Asn His His His 420	425	430	1296
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 Leu Ser Lys Lys Glu Leu Thr Leu Phe Ser Ile Ser Asn Phe Leu Ile 35 40 45			
 Met Ile Ala Val Thr Met Val Asn Val Asn Leu Phe Tyr Pro Ala Glu 50 55 60			

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65 70 75 80

Leu Ser Leu Asn Ile Phe Tyr Gly Leu Leu Pro Val Ala Ser Ser Asp  
85 90 95

Leu Phe Arg Arg Ala Ile Ile Phe Phe Ile Leu Asp Gly Thr Gln Gly  
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Ile Val Met Gly Ser Ser Ile Ile Thr Thr Tyr Met Ile Glu Phe Ala  
115 120 125

Gly Ile Ala Leu Ser Tyr Leu Phe Leu Ser Val Phe Asn Val Asp Ile  
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Gly Arg Leu Lys Asp Ser Leu Thr Lys Met Lys Val Lys Lys Arg Leu  
145 150 155 160

Ile Pro Met Asn Ile Thr Met Leu Leu Tyr Tyr Leu Leu Ile Gln Val  
165 170 175

Leu Tyr Val Ile Glu Ser Tyr Asn Val Ile Pro Thr Leu Lys Phe Arg  
180 185 190

Lys Phe Val Val Ile Val Tyr Leu Ile Leu Phe Leu Ile Leu Ile Ser  
195 200 205

Phe Leu Ser Gln Tyr Thr Lys Gln Lys Val Gln Asn Glu Ile Met Ala  
210 215 220

Gln Lys Glu Ala Gln Ile Arg Asn Ile Thr Gln Tyr Ser Gln Gln Ile  
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260 265 270

Ile Glu Lys Ile Tyr His Gln Ile Leu Glu Lys Thr Gly His Gln Leu  
275 280 285

Gln Asp Thr Arg Tyr Asn Ile Gly His Leu Ala Asn Ile Gln Asn Asp  
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Ala Ile Glu Ala Ala Phe Glu Ser Leu Asn Pro Glu Ile Gln Leu Ala  
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Phe Phe Lys Lys Asn Gly Ser Ile Val Phe Ile Ile Gln Asn Ser Thr  
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385 390 395 400

Thr Lys Gly Ser Asn Arg Gly Ile Gly Leu Ala Lys Val Asn His Ile  
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Leu Glu Thr Thr Ile Ala Ala Ile Met Lys Glu Lys Asn Trp Ser Tyr				
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aaa gaa ttg act att ttt gga aaa cca caa caa ctt att gac gct atc				144
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cct gaa aag ggc aat cac cag att ttc ttt ttg gat att gaa atc aaa				192
Pro Glu Lys Gly Asn His Gln Ile Phe Phe Leu Asp Ile Glu Ile Lys				
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aaa gag gaa aag aaa gga ctg gaa gta gcc aat cag att aga cag cat				240
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aat cct agt gca gtt att gtc ttt gtc acg aca cat tct gag ttt atg				288
Asn Pro Ser Ala Val Ile Val Phe Val Thr Thr His Ser Glu Phe Met				
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ccc ctc act ttt cag tat cag gta tct gct ttg gat ttt att gat aaa				336
Pro Leu Thr Phe Gln Tyr Gln Val Ser Ala Leu Asp Phe Ile Asp Lys				
100	105	110		
tct ttg aat cct gag gag ttc tcc cac cgc att gaa tca gcg ctg tat				384
Ser Leu Asn Pro Glu Glu Phe Ser His Arg Ile Glu Ser Ala Leu Tyr				
115	120	125		
tat gct atg gaa aac agc cag aag aat ggt caa tca gag gaa ctt ttt				432
Tyr Ala Met Glu Asn Ser Gln Lys Asn Gly Gln Ser Glu Glu Leu Phe				
130	135	140		
att ttc cat tca tct gaa act cag ttt cag gtc cct ttt gct gag att				480
Ile Phe His Ser Ser Glu Thr Gln Phe Gln Val Pro Phe Ala Glu Ile				
145	150	155	160	
ctg tat ttt gaa aca tct tca aca gcc cat aag ctc tgc ctt tat act				528
Leu Tyr Phe Glu Thr Ser Ser Thr Ala His Lys Leu Cys Leu Tyr Thr				
165	170	175		
tat gat gaa cgg att gaa ttc tac ggc agt atg act gac att gtt aaa				576
Tyr Asp Glu Arg Ile Glu Phe Tyr Gly Ser Met Thr Asp Ile Val Lys				
180	185	190		
atg gat aag aga ctt ttt cag tgc cat cgc tct ttt att gtc aat cct				624
Met Asp Lys Arg Leu Phe Gln Cys His Arg Ser Phe Ile Val Asn Pro				
195	200	205		
gcc aat att acc cgt att gat cgg aaa aaa cgc ttg gcc tat ttt cga				672
Ala Asn Ile Thr Arg Ile Asp Arg Lys Lys Arg Leu Ala Tyr Phe Arg				

210

215

220

aat aat aag tct tgt ctt att tca cga act aag tta aca aaa ctg aga  
Asn Asn Lys Ser Cys Leu Ile Ser Arg Thr Lys Leu Thr Lys Leu Arg  
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<212> PRT

<213> Streptococcus mutans

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Lys Glu Leu Thr Ile Phe Gly Lys Pro Gln Gln Leu Ile Asp Ala Ile  
35 40 45

Pro Glu Lys Gly Asn His Gln Ile Phe Phe Leu Asp Ile Glu Ile Lys  
50 55 60

Lys Glu Glu Lys Lys Gly Leu Glu Val Ala Asn Gln Ile Arg Gln His  
65 70 75 80

Asn Pro Ser Ala Val Ile Val Phe Val Thr Thr His Ser Glu Phe Met  
85 90 95

Pro Leu Thr Phe Gln Tyr Gln Val Ser Ala Leu Asp Phe Ile Asp Lys  
100 105 110

Ser Leu Asn Pro Glu Glu Phe Ser His Arg Ile Glu Ser Ala Leu Tyr  
115 120 125

Tyr Ala Met Glu Asn Ser Gln Lys Asn Gly Gln Ser Glu Glu Leu Phe  
130 135 140

Ile Phe His Ser Ser Glu Thr Gln Phe Gln Val Pro Phe Ala Glu Ile  
145 150 155 160

Leu Tyr Phe Glu Thr Ser Ser Thr Ala His Lys Leu Cys Leu Tyr Thr  
165 170 175

Tyr Asp Glu Arg Ile Glu Phe Tyr Gly Ser Met Thr Asp Ile Val Lys  
180 185 190

Met Asp Lys Arg Leu Phe Gln Cys His Arg Ser Phe Ile Val Asn Pro  
195 200 205

Ala Asn Ile Thr Arg Ile Asp Arg Lys Lys Arg Leu Ala Tyr Phe Arg  
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<211> 480

<212> DNA

<213> *Streptococcus mutans*

<220>

<221> CDS

<222> (1)..(408)

<400> 22  
atg gaa gaa gat ttt gaa att gtt ttt aat aag gtt aag cca att gta 48  
Met Glu Glu Asp Phe Glu Ile Val Phe Asn Lys Val Lys Pro Ile Val  
1 5 10 15

tgg aaa tta agc cgt tat tac ttt att aaa atg tgg act cgt gaa gat 96  
Trp Lys Leu Ser Arg Tyr Tyr Phe Ile Lys Met Trp Thr Arg Glu Asp  
20 25 30

tgg caa caa gag gga atg ttg att ttg cac caa tta tta agg gaa cat 144  
Trp Gln Gln Glu Gly Met Leu Ile Leu His Gln Leu Leu Arg Glu His  
35 40 45

cca gaa tta gaa gag gat gat aca aaa ttg tat atc tat ttt aag aca 192  
Pro Glu Leu Glu Asp Asp Thr Lys Leu Tyr Ile Tyr Phe Lys Thr  
50 55 60

cgt ttt tct aat tac att aaa gat gtt ttg cgt cag caa gaa agt cag 240  
Arg Phe Ser Asn Tyr Ile Lys Asp Val Leu Arg Gln Gln Glu Ser Gln  
65 70 75 80

aaa cgt cgt ttt aat aga atg tct tat gaa gaa gtc ggt gag att gaa 288  
Lys Arg Arg Phe Asn Arg Met Ser Tyr Glu Glu Val Gly Glu Ile Glu  
85 90 95

cac tgt ttg tca agt ggc ggt atg caa ttg gat gaa tat att tta ttt 336  
His Cys Leu Ser Ser Gly Gly Met Gln Leu Asp Glu Tyr Ile Leu Phe  
100 105 110

cgt gat agt ttg ctt gca tat aaa caa ggt ctg agt act gaa aag caa 384  
Arg Asp Ser Leu Leu Ala Tyr Lys Gln Gly Leu Ser Thr Glu Lys Gln  
115 120 125

gag ctg ttt gag cgc ttg gta gca ggagagcact ttttggaaag gcaaagtatg 438  
Glu Leu Phe Glu Arg Leu Val Ala  
130 135

ctgaaaagatt tacgtaaaaa attaagtgtat tttaaggaaa aa 480

<210> 23

<211> 136

<212> PRT

<213> Streptococcus mutans

<400> 23

Met Glu Glu Asp Phe Glu Ile Val Phe Asn Lys Val Lys Pro Ile Val

1

5

10

15

Trp Lys Leu Ser Arg Tyr Tyr Phe Ile Lys Met Trp Thr Arg Glu Asp  
20 25 30

Trp Gln Gln Glu Gly Met Leu Ile Leu His Gln Leu Leu Arg Glu His  
35 40 45

Pro Glu Leu Glu Glu Asp Asp Thr Lys Leu Tyr Ile Tyr Phe Lys Thr  
50 55 60

Arg Phe Ser Asn Tyr Ile Lys Asp Val Leu Arg Gln Gln Glu Ser Gln  
65 70 75 80

Lys Arg Arg Phe Asn Arg Met Ser Tyr Glu Glu Val Gly Glu Ile Glu  
85 90 95

His Cys Leu Ser Ser Gly Gly Met Gln Leu Asp Glu Tyr Ile Leu Phe  
100 105 110

Arg Asp Ser Leu Leu Ala Tyr Lys Gln Gly Leu Ser Thr Glu Lys Gln  
115 120 125

Glu Leu Phe Glu Arg Leu Val Ala  
130 135

<210> 24

<211> 680

<212> DNA

<213> *Streptococcus mutans*

<220>

<221> misc\_feature

<222> (1)..(680)

<400> 24

gtaaataaaaa cagccagtta agatgggaca tttatgtcct gttcttaaag tctttttcgt 60

tttataataa ttttattata aaaggaggtc atcgtaatag atggaagaag attttgaat 120

tgtttttaat aaggtaagc caattgtatg gaaattaagc cgttattact ttat	180
gtggactcgt gaagattggc aacaagaggg aatgttgatt ttgcaccaat tattaaggga	240
acatccagaa ttagaagagg atgatacaa attgtatatac tatttaaga cacgttttc	300
taattacatt aaagatgtt tgcgtcagca agaaagtcag aaacgtcggt ttaatagaat	360
gtcttatgaa gaagtcggtg agattgaaca ctgttgtca agtggcggt tgcaattgga	420
tgaatatatt ttatttcgtg atagttgct tgcatataaa caaggctctga gtactgaaaa	480
gcaagagctg tttgagcgct tggtagcagg agagcacttt ttgggaaggc aaagtatgct	540
gaaagattt cgtaaaaat taagtgatt taagaaaaa tagttaaaaa gggaaagaat	600
ggaacatgtg attgtaccat tcttttggt tgaaaattaa gaaaagttat tataaattat	660
tggttaaca tgccatatta	680

<210> 25

<211> 2280

<212> DNA

<213> Streptococcus mutans

<220>

<221> CDS

<222> (1) .. (2280)

<400> 25

atg aaa caa gtt att tat gtt gtt tta atc gtc ata gcc gtt aac att	48
Met Lys Gln Val Ile Tyr Val Val Leu Ile Val Ile Ala Val Asn Ile	
1 5 10 15	

ctc tta gag att atc aaa aga gta aca aaa agg gga ggg aca gtt tcg	96
Leu Leu Glu Ile Ile Lys Arg Val Thr Lys Arg Gly Gly Thr Val Ser	
20 25 30	

tca tct aat cct tta cca gat ggg cag tct aag ttg ttt tgg cgc aga	144
Ser Ser Asn Pro Leu Pro Asp Gly Gln Ser Lys Leu Phe Trp Arg Arg	
35 40 45	

cat tat aag cta gta cct cag att gat acc aga gac tgt ggg ccg gca	192
His Tyr Lys Leu Val Pro Gln Ile Asp Thr Arg Asp Cys Gly Pro Ala	
50 55 60	

gtg ctg gca tct gtt gca aag cat tac gga tct aat tac tct atc gct			240
Val Leu Ala Ser Val Ala Lys His Tyr Gly Ser Asn Tyr Ser Ile Ala			
65	70	75	80
tat ctg cgg gaa ctc tca aag act aac aag cag gga aca aca gct ctt			288
Tyr Leu Arg Glu Leu Ser Lys Thr Asn Lys Gln Gly Thr Thr Ala Leu			
85	90	95	
ggc att gtt gaa gct gct aaa aag tta ggc ttt gaa aca cgc tct atc			336
Gly Ile Val Glu Ala Ala Lys Lys Leu Gly Phe Glu Thr Arg Ser Ile			
100	105	110	
aag gcg gat atg acg ctt ttt gat tat aat gat ttg acc tat cct ttt			384
Lys Ala Asp Met Thr Leu Phe Asp Tyr Asn Asp Leu Thr Tyr Pro Phe			
115	120	125	
atc gtc cat gtg att aaa gga aaa cgt ctg cag cat tat tat gtc gtc			432
Ile Val His Val Ile Lys Gly Lys Arg Leu Gln His Tyr Tyr Val Val			
130	135	140	
tat ggc agc cag aat aat cag ctg att att gga gat cct gat cct tca			480
Tyr Gly Ser Gln Asn Asn Gln Leu Ile Ile Gly Asp Pro Asp Pro Ser			
145	150	155	160
gtt aag gtg act agg atg agt aag gaa cgc ttt caa tca gag tgg aca			528
Val Lys Val Thr Arg Met Ser Lys Glu Arg Phe Gln Ser Glu Trp Thr			
165	170	175	
ggc ctt gca att ttc cta gct cct cag cct aac tat aag cct cat aaa			576
Gly Leu Ala Ile Phe Leu Ala Pro Gln Pro Asn Tyr Lys Pro His Lys			
180	185	190	
ggt gaa aaa aat ggt ttg tct aat ttc ttc ccg ttg atc ttt aag cag			624
Gly Glu Lys Asn Gly Leu Ser Asn Phe Phe Pro Leu Ile Phe Lys Gln			
195	200	205	
aaa gct ttg atg act tat att atc ata gct agc ttg att gtg acg ctc			672
Lys Ala Leu Met Thr Tyr Ile Ile Ala Ser Leu Ile Val Thr Leu			
210	215	220	
att gat att gtc gga tca tac tat ctc caa gga ata ttg gac gag tac			720
Ile Asp Ile Val Gly Ser Tyr Tyr Leu Gln Gly Ile Leu Asp Glu Tyr			
225	230	235	240
att cct gat cag ctg att tca act tta gga atg att acg att ggt ctg			768
Ile Pro Asp Gln Leu Ile Ser Thr Leu Gly Met Ile Thr Ile Gly Leu			
245	250	255	
ata ata acc tat att atc cag cag gtc atg gct ttt gca aaa gaa tac			816
Ile Ile Thr Tyr Ile Ile Gln Gln Val Met Ala Phe Ala Lys Glu Tyr			
260	265	270	
ctc ttg gcc gta ctc agt ttg cgt tta gtc att gat gtt atc ctg tct			864
Leu Leu Ala Val Leu Ser Leu Arg Leu Val Ile Asp Val Ile Leu Ser			
275	280	285	
tat atc aaa cat att ttt acg ctt cct atg tct ttc ttt gcg aca agg			912

Tyr Ile Lys His Ile Phe Thr Leu Pro Met Ser Phe Phe Ala Thr Arg			
290	295	300	
cg aca gga gaa atc acg tct cgt ttt aca gat gcc aat cag att att			960
Arg Thr Gly Glu Ile Thr Ser Arg Phe Thr Asp Ala Asn Gln Ile Ile			
305	310	315	320
gat gct gta gcg tca acc atc ttt tca atc ttt tta gat atg act atg			1008
Asp Ala Val Ala Ser Thr Ile Phe Ser Ile Phe Leu Asp Met Thr Met			
325	330	335	
gta att ttg gtt ggt ggg gtt ttg ttg gcg caa aac aat aac ctt ttc			1056
Val Ile Leu Val Gly Gly Val Leu Leu Ala Gln Asn Asn Asn Leu Phe			
340	345	350	
ttt cta acc ttg ctc tcc att ccg att tat gcc atc att att ttt gct			1104
Phe Leu Thr Leu Leu Ser Ile Pro Ile Tyr Ala Ile Ile Ile Phe Ala			
355	360	365	
ttc ttg aaa ccc ttt gag aaa atg aat cac gaa gtg atg gaa agc aat			1152
Phe Leu Lys Pro Phe Glu Lys Met Asn His Glu Val Met Glu Ser Asn			
370	375	380	
gct gtg gta agt tct atc att gaa gat atc aat ggg atg gaa acc			1200
Ala Val Val Ser Ser Ile Ile Glu Asp Ile Asn Gly Met Glu Thr			
385	390	395	400
att aaa tca ctc aca agt gag tcc gct cgt tat caa aac att gat agt			1248
Ile Lys Ser Leu Thr Ser Glu Ser Ala Arg Tyr Gln Asn Ile Asp Ser			
405	410	415	
gaa ttt gtt gat tat ttg gag aaa aac ttt aag cta cac aag tat agt			1296
Glu Phe Val Asp Tyr Leu Glu Lys Asn Phe Lys Leu His Lys Tyr Ser			
420	425	430	
gcc att caa acc gca tta aaa agc ggt gct aag ctt atc ctc aat gtt			1344
Ala Ile Gln Thr Ala Leu Lys Ser Gly Ala Lys Leu Ile Leu Asn Val			
435	440	445	
gtc att ctc tgg tat ggc tct cgt cta gtt atg gat aat aaa atc tca			1392
Val Ile Leu Trp Tyr Gly Ser Arg Leu Val Met Asp Asn Lys Ile Ser			
450	455	460	
gtt ggt cag ctt atc acc ttt aat gct ttg ctg tct tat ttc tca aat			1440
Val Gly Gln Leu Ile Thr Phe Asn Ala Leu Leu Ser Tyr Phe Ser Asn			
465	470	475	480
cca att gaa aat att atc aat ctg caa tcc aaa ctg cag tca gct cgc			1488
Pro Ile Glu Asn Ile Ile Asn Leu Gln Ser Lys Leu Gln Ser Ala Arg			
485	490	495	
gtt gcc aat aca cgt ctt aat gag gtc tat ctt gtc gaa tct gaa ttt			1536
Val Ala Asn Thr Arg Leu Asn Glu Val Tyr Leu Val Glu Ser Glu Phe			
500	505	510	
gaa aaa gac ggc gat tta tca gaa aat agc ttt tta gat ggt gat att			1584
Glu Lys Asp Gly Asp Leu Ser Glu Asn Ser Phe Leu Asp Gly Asp Ile			

DRAFT

515	520	525	
tcg ttt gaa aat ctt tct tat aaa tat gga ttt ggg cga gat acc tta Ser Phe Glu Asn Leu Ser Tyr Lys Tyr Gly Phe Gly Arg Asp Thr Leu 530	535	540	1632
tca gat att aat tta tca atc aaa aaa ggc tcc aag gtc agt cta gtt Ser Asp Ile Asn Leu Ser Ile Lys Lys Gly Ser Lys Val Ser Leu Val 545	550	555	1680
gga gcc agt ggt tct ggt aaa aca act ttg gct aaa ctg att gtc aat Gly Ala Ser Gly Ser Gly Lys Thr Thr Leu Ala Lys Leu Ile Val Asn 565	570	575	1728
ttc tac gag cct aac aag ggg att gtt cga atc aat ggc aat gat tta Phe Tyr Glu Pro Asn Lys Gly Ile Val Arg Ile Asn Gly Asn Asp Leu 580	585	590	1776
aaa gtt att gat aag aca gct ttg cgg cgg cat att agc tat ttg ccg Lys Val Ile Asp Lys Thr Ala Leu Arg Arg His Ile Ser Tyr Leu Pro 595	600	605	1824
caa cag gcc tat gtt ttt agt ggc tct att atg gat aat ctc gtt tta Gln Gln Ala Tyr Val Phe Ser Gly Ser Ile Met Asp Asn Leu Val Leu 610	615	620	1872
gga gct aaa gaa gga acg agt cag gaa gac att att cgt gct tgt gaa Gly Ala Lys Glu Gly Thr Ser Gln Glu Asp Ile Ile Arg Ala Cys Glu 625	630	635	1920
att gct gaa atc cgc tcg gac att gaa caa atg cct cag ggc tat cag Ile Ala Glu Ile Arg Ser Asp Ile Glu Gln Met Pro Gln Gly Tyr Gln 645	650	655	1968
aca gag tta tca gat ggt gcc ggt att tct ggc ggt caa aaa cag cgg Thr Glu Leu Ser Asp Gly Ala Gly Ile Ser Gly Gly Gln Lys Gln Arg 660	665	670	2016
att gct tta gct agg gcc tta tta aca cag gca ccg gtt ttg att ctg Ile Ala Leu Ala Arg Ala Leu Leu Thr Gln Ala Pro Val Leu Ile Leu 675	680	685	2064
gat gaa gcc acc agc agt ctt gat att ttg aca gaa aag aaa att atc Asp Glu Ala Thr Ser Ser Leu Asp Ile Leu Thr Glu Lys Lys Ile Ile 690	695	700	2112
agc aat ctc tta cag atg acg gag aaa aca ata att ttt gtt gcc cac Ser Asn Leu Leu Gln Met Thr Glu Lys Thr Ile Ile Phe Val Ala His 705	710	715	2160
cgc tta agc att tca cag cgt act gac gaa gtc att gtc atg gat cag Arg Leu Ser Ile Ser Gln Arg Thr Asp Glu Val Ile Val Met Asp Gln 725	730	735	2208
gga aaa att gtt gaa caa ggc act cat aag gaa ctt tta gct aag caa Gly Lys Ile Val Glu Gln Gly Thr His Lys Glu Leu Leu Ala Lys Gln 740	745	750	2256

ggt ttc tat tat aac ctg ttt aat  
Gly Phe Tyr Tyr Asn Leu Phe Asn  
755 760

2280

<210> 26

<211> 760

<212> PRT

<213> Streptococcus mutans

<400> 26

Met Lys Gln Val Ile Tyr Val Val Leu Ile Val Ile Ala Val Asn Ile  
1 5 10 15

Leu Leu Glu Ile Ile Lys Arg Val Thr Lys Arg Gly Gly Thr Val Ser  
20 25 30

Ser Ser Asn Pro Leu Pro Asp Gly Gln Ser Lys Leu Phe Trp Arg Arg  
35 40 45

His Tyr Lys Leu Val Pro Gln Ile Asp Thr Arg Asp Cys Gly Pro Ala  
50 55 60

Val Leu Ala Ser Val Ala Lys His Tyr Gly Ser Asn Tyr Ser Ile Ala  
65 70 75 80

Tyr Leu Arg Glu Leu Ser Lys Thr Asn Lys Gln Gly Thr Thr Ala Leu  
85 90 95

Gly Ile Val Glu Ala Ala Lys Lys Leu Gly Phe Glu Thr Arg Ser Ile  
100 105 110

Lys Ala Asp Met Thr Leu Phe Asp Tyr Asn Asp Leu Thr Tyr Pro Phe  
115 120 125

Ile Val His Val Ile Lys Gly Lys Arg Leu Gln His Tyr Tyr Val Val  
130 135 140

Tyr Gly Ser Gln Asn Asn Gln Leu Ile Ile Gly Asp Pro Asp Pro Ser  
145 150 155 160

Val Lys Val Thr Arg Met Ser Lys Glu Arg Phe Gln Ser Glu Trp Thr  
165 170 175

Gly Leu Ala Ile Phe Leu Ala Pro Gln Pro Asn Tyr Lys Pro His Lys  
180 185 190

Gly Glu Lys Asn Gly Leu Ser Asn Phe Phe Pro Leu Ile Phe Lys Gln  
195 200 205

Lys Ala Leu Met Thr Tyr Ile Ile Ile Ala Ser Leu Ile Val Thr Leu  
210 215 220

Ile Asp Ile Val Gly Ser Tyr Tyr Leu Gln Gly Ile Leu Asp Glu Tyr  
225 230 235 240

Ile Pro Asp Gln Leu Ile Ser Thr Leu Gly Met Ile Thr Ile Gly Leu  
245 250 255

Ile Ile Thr Tyr Ile Ile Gln Gln Val Met Ala Phe Ala Lys Glu Tyr  
260 265 270

Leu Leu Ala Val Leu Ser Leu Arg Leu Val Ile Asp Val Ile Leu Ser  
275 280 285

Tyr Ile Lys His Ile Phe Thr Leu Pro Met Ser Phe Phe Ala Thr Arg  
290 295 300

Arg Thr Gly Glu Ile Thr Ser Arg Phe Thr Asp Ala Asn Gln Ile Ile  
305 310 315 320

Asp Ala Val Ala Ser Thr Ile Phe Ser Ile Phe Leu Asp Met Thr Met  
325 330 335

Val Ile Leu Val Gly Gly Val Leu Leu Ala Gln Asn Asn Asn Leu Phe  
340 345 350

Phe Leu Thr Leu Leu Ser Ile Pro Ile Tyr Ala Ile Ile Ile Phe Ala  
355 360 365

Phe Leu Lys Pro Phe Glu Lys Met Asn His Glu Val Met Glu Ser Asn  
370 375 380

Ala Val Val Ser Ser Ser Ile Ile Glu Asp Ile Asn Gly Met Glu Thr  
385 390 395 400

Ile Lys Ser Leu Thr Ser Glu Ser Ala Arg Tyr Gln Asn Ile Asp Ser  
405 410 415

Glu Phe Val Asp Tyr Leu Glu Lys Asn Phe Lys Leu His Lys Tyr Ser  
420 425 430

Ala Ile Gln Thr Ala Leu Lys Ser Gly Ala Lys Leu Ile Leu Asn Val  
435 440 445

Val Ile Leu Trp Tyr Gly Ser Arg Leu Val Met Asp Asn Lys Ile Ser  
450 455 460

Val Gly Gln Leu Ile Thr Phe Asn Ala Leu Leu Ser Tyr Phe Ser Asn  
465 470 475 480

Pro Ile Glu Asn Ile Ile Asn Leu Gln Ser Lys Leu Gln Ser Ala Arg  
485 490 495

Val Ala Asn Thr Arg Leu Asn Glu Val Tyr Leu Val Glu Ser Glu Phe  
500 505 510

Glu Lys Asp Gly Asp Leu Ser Glu Asn Ser Phe Leu Asp Gly Asp Ile  
515 520 525

Ser Phe Glu Asn Leu Ser Tyr Lys Tyr Gly Phe Gly Arg Asp Thr Leu  
530 535 540

Ser Asp Ile Asn Leu Ser Ile Lys Lys Gly Ser Lys Val Ser Leu Val  
545 550 555 560

Gly Ala Ser Gly Ser Gly Lys Thr Thr Leu Ala Lys Leu Ile Val Asn  
565 570 575

Phe Tyr Glu Pro Asn Lys Gly Ile Val Arg Ile Asn Gly Asn Asp Leu  
580 585 590

Lys Val Ile Asp Lys Thr Ala Leu Arg Arg His Ile Ser Tyr Leu Pro  
595 600 605

Gln Gln Ala Tyr Val Phe Ser Gly Ser Ile Met Asp Asn Leu Val Leu

610

615

620

Gly Ala Lys Glu Gly Thr Ser Gln Glu Asp Ile Ile Arg Ala Cys Glu  
625 630 635 640

Ile Ala Glu Ile Arg Ser Asp Ile Glu Gln Met Pro Gln Gly Tyr Gln  
645 650 655

Thr Glu Leu Ser Asp Gly Ala Gly Ile Ser Gly Gly Gln Lys Gln Arg  
660 665 670

Ile Ala Leu Ala Arg Ala Leu Leu Thr Gln Ala Pro Val Leu Ile Leu  
675 680 685

Asp Glu Ala Thr Ser Ser Leu Asp Ile Leu Thr Glu Lys Lys Ile Ile  
690 695 700

Ser Asn Leu Leu Gln Met Thr Glu Lys Thr Ile Ile Phe Val Ala His  
705 710 715 720

Arg Leu Ser Ile Ser Gln Arg Thr Asp Glu Val Ile Val Met Asp Gln  
725 730 735

Gly Lys Ile Val Glu Gln Gly Thr His Lys Glu Leu Leu Ala Lys Gln  
740 745 750

Gly Phe Tyr Tyr Asn Leu Phe Asn  
755 760

<210> 27

<211> 900

<212> DNA

<213> Streptococcus mutans

<220>

<221> CDS

<222> (1)..(900)

<400> 27			
atg gat cct aaa ttt tta caa agt gca gaa ttt tat agg aga cgc tat			48
Met Asp Pro Lys Phe Leu Gln Ser Ala Glu Phe Tyr Arg Arg Arg Tyr			
1 5 10 15			
cat aat ttt gcg aca cta tta att gtt cct ttg gtc tgc ttg att atc			96
His Asn Phe Ala Thr Leu Leu Ile Val Pro Leu Val Cys Leu Ile Ile			
20 25 30			
ttc ttg gtc ata ttc ctt tgt ttt gct aaa aaa gaa att aca gtg att			144
Phe Leu Val Ile Phe Leu Cys Phe Ala Lys Lys Glu Ile Thr Val Ile			
35 40 45			
tct act ggt gaa gtt gca cca aca aag gtt gta gat gtt atc caa tct			192
Ser Thr Gly Glu Val Ala Pro Thr Lys Val Val Asp Val Ile Gln Ser			
50 55 60			
tac agt gac agt tca atc att aaa aat aat tta gat aat aat gca gct			240
Tyr Ser Asp Ser Ser Ile Ile Lys Asn Asn Leu Asp Asn Asn Ala Ala			
65 70 75 80			
gtt gag aag gga gac gtt tta att gaa tat tca gaa aat gcc agt cca			288
Val Glu Lys Gly Asp Val Leu Ile Glu Tyr Ser Glu Asn Ala Ser Pro			
85 90 95			
aac cgt cag act gaa caa aag aat att ata aaa gaa aga caa aaa cga			336
Asn Arg Gln Thr Glu Gln Lys Asn Ile Ile Lys Glu Arg Gln Lys Arg			
100 105 110			
gaa gag aag gaa aag aaa aaa cac caa aag agc aag aaa aag aag aag			384
Glu Glu Lys Glu Lys Lys Lys His Gln Lys Ser Lys Lys Lys Lys Lys			
115 120 125			
tct aag agc aag aaa gct tcc aaa gat aag aaa aag aaa tcg aaa gac			432
Ser Lys Ser Lys Ala Ser Lys Asp Lys Lys Lys Ser Lys Asp			
130 135 140			
aag gaa agc agc tct gac gat gaa aat gag aca aaa aag gtt tcg att			480
Lys Glu Ser Ser Asp Asp Glu Asn Glu Thr Lys Lys Val Ser Ile			
145 150 155 160			
ttt gct tca gaa gat ggt att att cat acc aat ccc aaa tat gat ggt			528
Phe Ala Ser Glu Asp Gly Ile Ile His Thr Asn Pro Lys Tyr Asp Gly			
165 170 175			
gcc aat att att ccg aag caa acc gag att gct caa atc tat cct gat			576
Ala Asn Ile Ile Pro Lys Gln Thr Glu Ile Ala Gln Ile Tyr Pro Asp			
180 185 190			
att caa aaa aca aga aaa gtg tta atc acc tat tat gct tct tct gat			624
Ile Gln Lys Thr Arg Lys Val Leu Ile Thr Tyr Tyr Ala Ser Ser Asp			
195 200 205			
gat gtt gtt tct atg aaa aag ggg caa acc gct cgt ctt tcc ttg gaa			672
Asp Val Val Ser Met Lys Lys Gly Gln Thr Ala Arg Leu Ser Leu Glu			
210 215 220			

aaa aag gga aat gac aag gtt gtt att gaa gga aaa att aac aat gtc	720
Lys Lys Gly Asn Asp Lys Val Val Ile Glu Gly Lys Ile Asn Asn Val	
225 230 235 240	
gct tca tca gca act act act aaa aaa gga aat ctc ttt aag gtt act	768
Ala Ser Ser Ala Thr Thr Lys Lys Gly Asn Leu Phe Lys Val Thr	
245 250 255	
gcc aaa gta aag gtt tct aag aaa aat agc aaa ctc atc aag tat ggt	816
Ala Lys Val Lys Val Ser Lys Lys Asn Ser Lys Leu Ile Lys Tyr Gly	
260 265 270	
atg aca ggc aag aca gtc act gtc att gat aaa aag act tat ttt gat	864
Met Thr Gly Lys Thr Val Thr Val Ile Asp Lys Lys Thr Tyr Phe Asp	
275 280 285	
tat ttc aaa gat aaa tta ctg cat aaa atg gat aat	900
Tyr Phe Lys Asp Lys Leu Leu His Lys Met Asp Asn	
290 295 300	

<210> 28

<211> 300

<212> PRT

<213> Streptococcus mutans

<400> 28

Met Asp Pro Lys Phe Leu Gln Ser Ala Glu Phe Tyr Arg Arg Arg Tyr	
1 5 10 15	

His Asn Phe Ala Thr Leu Leu Ile Val Pro Leu Val Cys Leu Ile Ile	
20 25 30	

Phe Leu Val Ile Phe Leu Cys Phe Ala Lys Lys Glu Ile Thr Val Ile	
35 40 45	

Ser Thr Gly Glu Val Ala Pro Thr Lys Val Val Asp Val Ile Gln Ser	
50 55 60	

Tyr Ser Asp Ser Ser Ile Ile Lys Asn Asn Leu Asp Asn Asn Ala Ala	
65 70 75 80	

Val Glu Lys Gly Asp Val Leu Ile Glu Tyr Ser Glu Asn Ala Ser Pro	
85 90 95	

Asn Arg Gln Thr Glu Gln Lys Asn Ile Ile Lys Glu Arg Gln Lys Arg  
100 105 110

Glu Glu Lys Glu Lys Lys His Gln Lys Ser Lys Lys Lys Lys Lys  
115 120 125

Ser Lys Ser Lys Lys Ala Ser Lys Asp Lys Lys Lys Ser Lys Asp  
130 135 140

Lys Glu Ser Ser Asp Asp Glu Asn Glu Thr Lys Lys Val Ser Ile  
145 150 155 160

Phe Ala Ser Glu Asp Gly Ile Ile His Thr Asn Pro Lys Tyr Asp Gly  
165 170 175

Ala Asn Ile Ile Pro Lys Gln Thr Glu Ile Ala Gln Ile Tyr Pro Asp  
180 185 190

Ile Gln Lys Thr Arg Lys Val Leu Ile Thr Tyr Tyr Ala Ser Ser Asp  
195 200 205

Asp Val Val Ser Met Lys Lys Gly Gln Thr Ala Arg Leu Ser Leu Glu  
210 215 220

Lys Lys Gly Asn Asp Lys Val Val Ile Glu Gly Lys Ile Asn Asn Val  
225 230 235 240

Ala Ser Ser Ala Thr Thr Lys Lys Gly Asn Leu Phe Lys Val Thr  
245 250 255

Ala Lys Val Lys Val Ser Lys Lys Asn Ser Lys Leu Ile Lys Tyr Gly  
260 265 270

Met Thr Gly Lys Thr Val Thr Val Ile Asp Lys Lys Thr Tyr Phe Asp  
275 280 285

Tyr Phe Lys Asp Lys Leu Leu His Lys Met Asp Asn  
290 295 300